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<pre>GAACTTCTCAGAGAATGCTCCAAAACCTCAGCAGTGCCTTCTGGTGGTGAATCAGTGCT</pre>	<pre>TCTGCAACCCATGAGGCCGGAGCAGAAATGACTCTGTGAGCCCCAGGAAATCCCAGTGGCG</pre>	<pre>GCCCARAACTCAGCTGAAGTGGTTCTGCCTCAACAGTCCTACAGGTGGCTGGCG</pre>	<pre>GCTTTTGCATGCCAAGACTCCACCTGACACAGATGGCATGCTATGACATCTGTAAA</pre>	<pre>TCCCTCTGATACGGGCTGCTAATTGACACTCAGGGAAARGCATTCGTCAAAGAGAGC</pre>
1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAla	16 SerAlaThrHisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAla	36 AlaGlnAsnSerAlaGluValAlaValArgCysLeuAsnSerAlaLeuGlnValGlyCysGly	56 AlaPheAlaCysLeuGluGlnSerThrCysAspThrAspGlyXetTyrrAspIleCysLys	

FIG. 1A

MATCH WITH FIG.1B

MATCH WITH FIG.1A

76 SerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSer 95
TTAAATGCATGCCAACGGGTCAACCTCCAAAGTCCTCCTGCCATTGGAGGTGCTCC
+-----+-----+-----+-----+-----+-----+-----+-----+
96 LeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSer 115
ACTTTCCAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC
+-----+-----+-----+-----+-----+-----+-----+-----+
116 ThrPheGlnArgMetIleAlaGluValGlnGluCystyrSerLysLeuAsnValCys 135
AGCATCGCCAAGGGAACCCCTGAAGCCATCACTGAGGTCGTCAGCTGCCAAATCACTTC
+-----+-----+-----+-----+-----+-----+-----+-----+
136 SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe 155
TCCAAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGATGTGATGAAGACACAGTC
+-----+-----+-----+-----+-----+-----+-----+-----+
156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal 175

MATCH WITH FIG.1C

FIG. 1B

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MATCH WITH FIG.1B

AGCACAAATCAGAGACAGCCTGATCGAGAAAATTGGGCCATAACATGGCCAGCCTCTTCCAC
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195

ATCCTGCAGAACGACCAACTGTGCCAAACACACCACGGAGCTGACTTCACAGGAGACGCC
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
196 IleLeuGlnThrAspHisCysAlaIleGlnThrHisProArgAlaAspPheAsnArgArgArg 215

ACCAATGAGCCGAGAAGCTGAAGTCCTCCTCAGGAACCTCCGAGGTGAGGGACTCT
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
216 ThrAsnGluProGlnLysLeuLeuValLeuArgAsnLeuArgGlyGluGluAspSer 235

CCCTCCCCACATCAACGGCACATCCCCATGAGAGTCCATAACCCAGGGAGGGT
+-----+-----+-----+-----+-----+-----+-----+-----+-----+
236 ProSerHisIleIleArgThrSerHisGluSerAla 247

FIG. 1C

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MHQNSAVLLVVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL
ML + V ++ +A + SPR+ +R ++ + +V RCLN AL VGCG FACL
MLAKFGGLCAVFLVLGTAATFDTDPEEASPRRARFSSNSPSDVARCLNGALA VGGTFACL

ENSTCDTDGMYDICKSELYSAAKEDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM
ENSTCDTDGM+DIC+ F +AA F+TQGK FVKESL+CIANGVTSKVF IRRC FORM
ENSTCDTDGMHDICQLEFFHTATENTQGKTFVKESLRCIAANGVTSKVFQTIRRCGVFQRM

IAEVQEECYSKLNVCASIAKRNPEAITEVVQLPNHFSNRYYNRILVRSLLIECDEDTVSTIRD
I+EVQEECY S+L++C +A+ NPEAI EVVQ+P HF NRYY+ L++SLL CDE+TV+ +R
ISEVQEECYSRILDICGVARSNPERAIGEVVQVPAHFPNRYYSTILLQSLLLACDEETVAVVRA

SLMEKIGPNMASLFHILQTDHCAQ
L+ ++GP+M +LF +LQ HC Q
GLVARLGPDMETLTFQLLQNKHCPQ 204

FIG.2

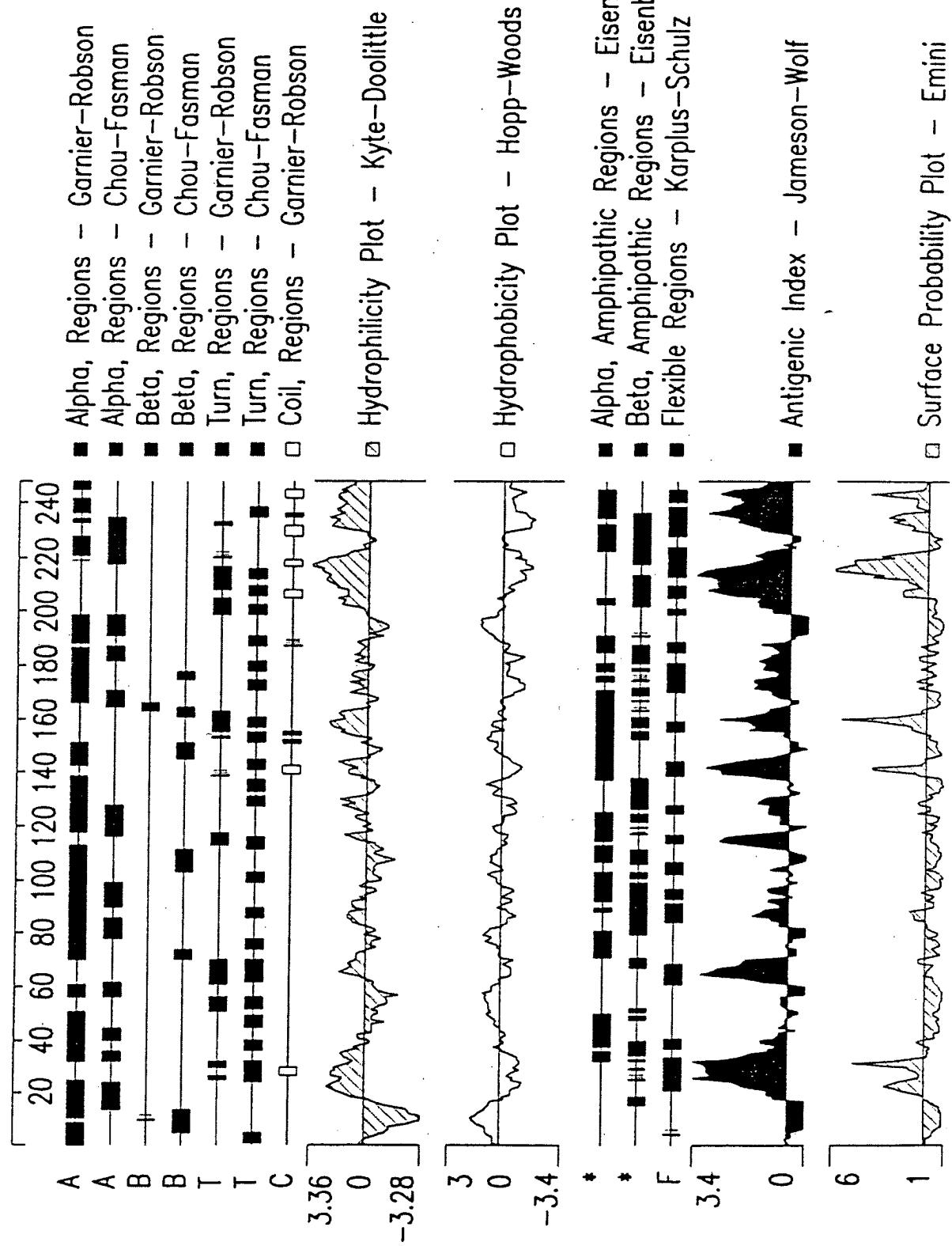


FIG. 3

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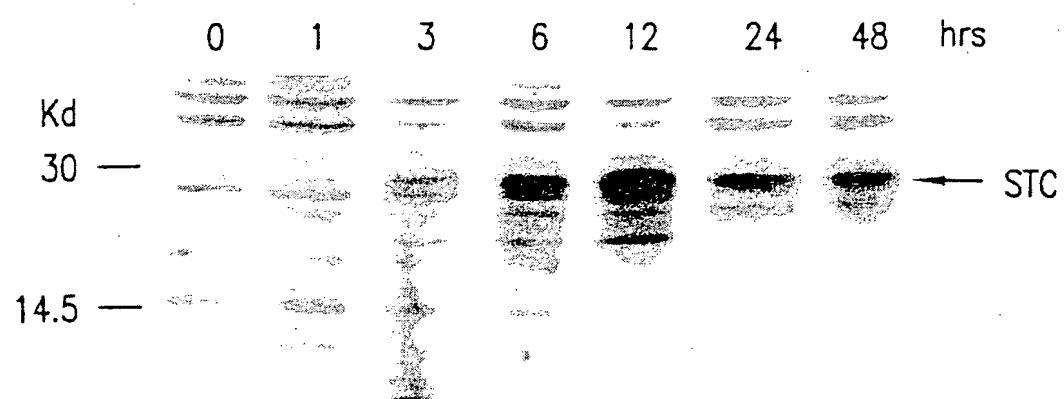


FIG.4

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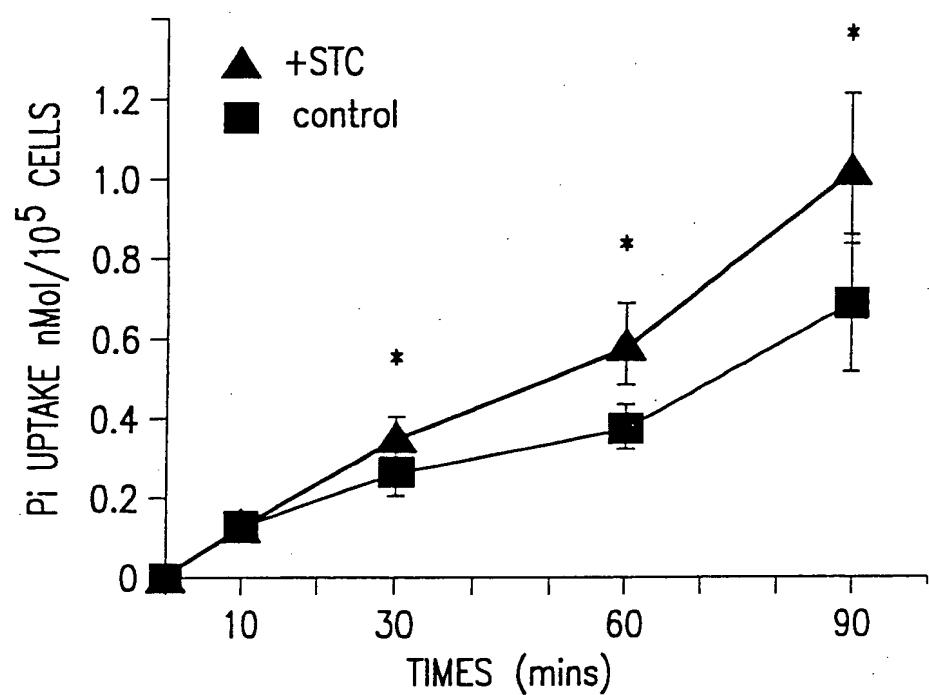


FIG.5

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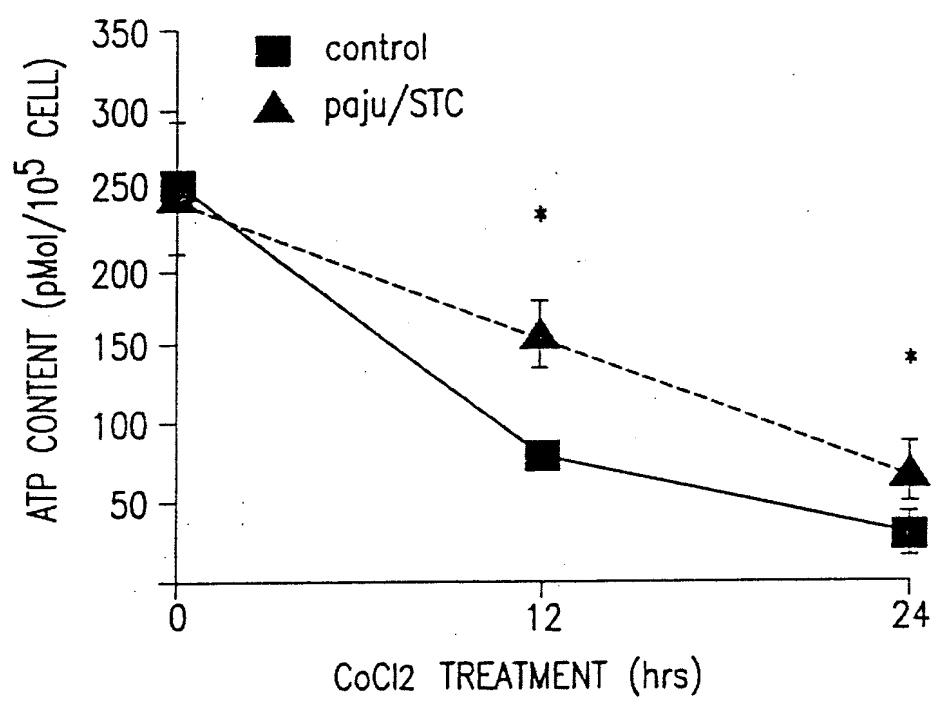
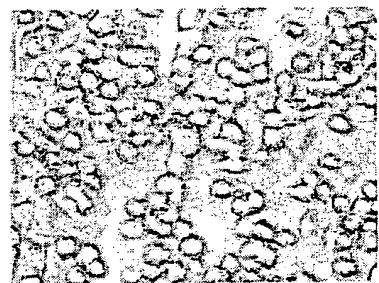


FIG.6

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Paju/C



Paju/STC

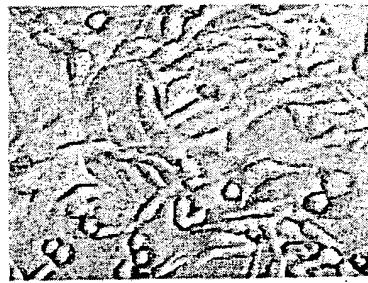


FIG.7A

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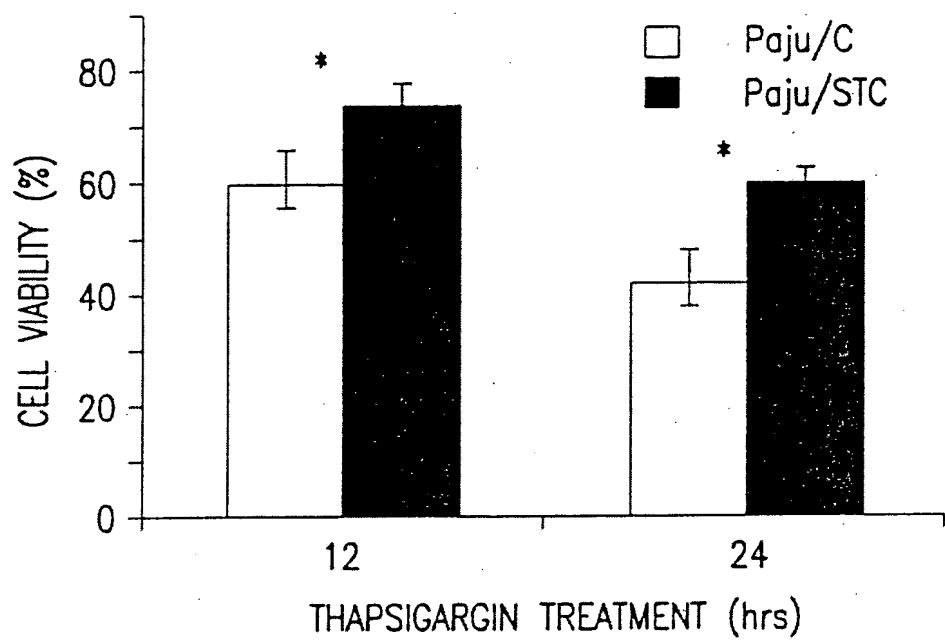


FIG. 7B

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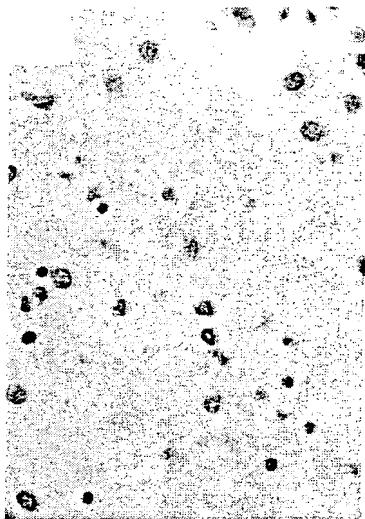


FIG.8A

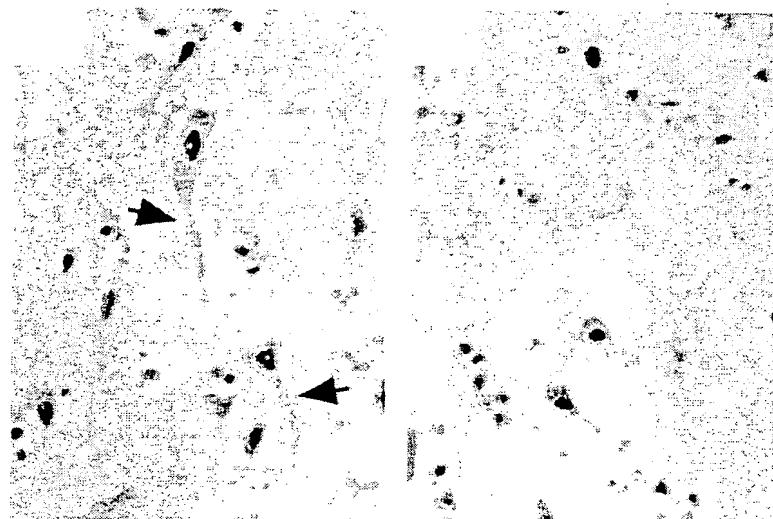


FIG.8B

FIG.8C

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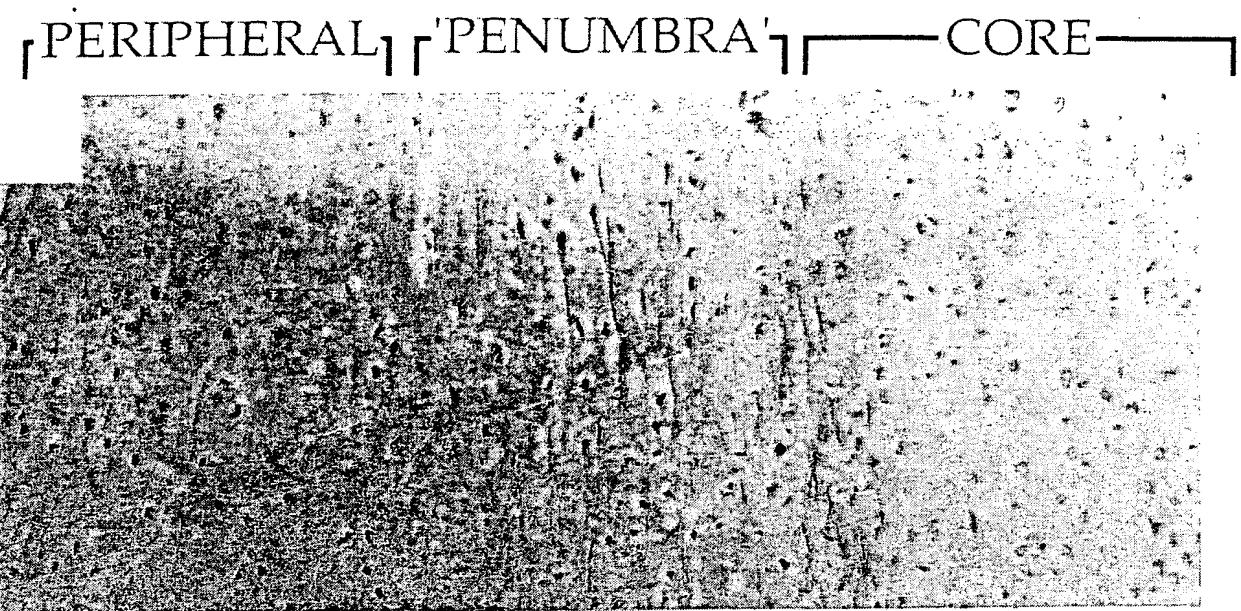


FIG.9A

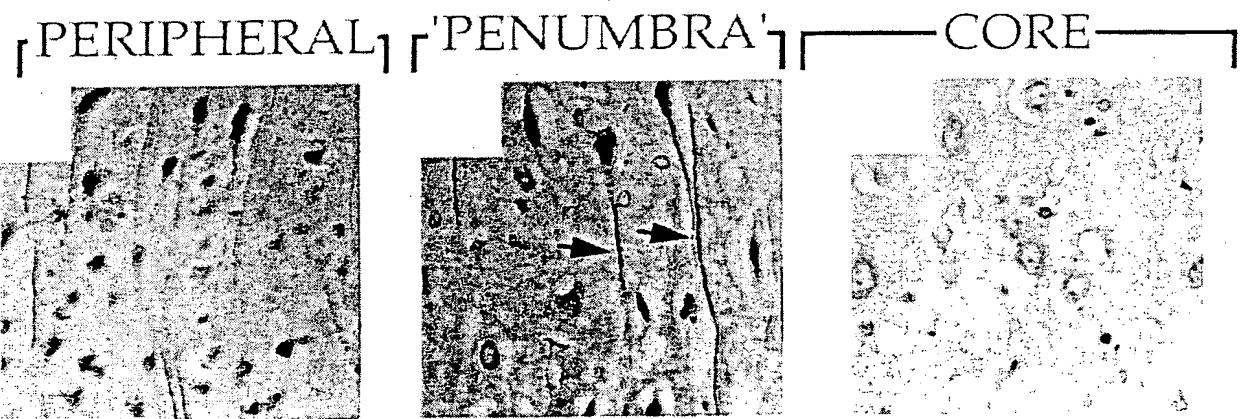


FIG.9B

FIG.9C

FIG.9D